

IV

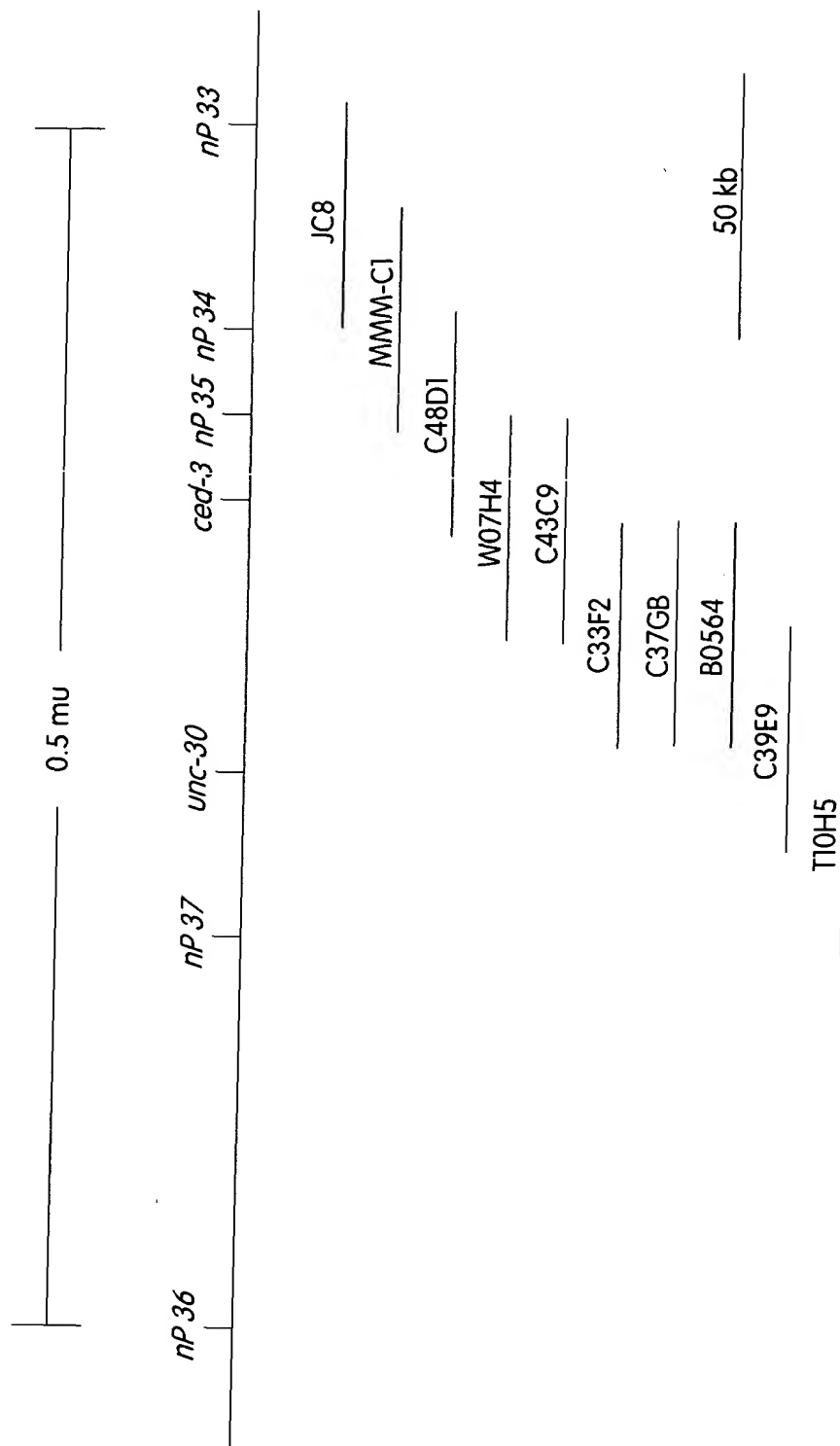


Fig. 1

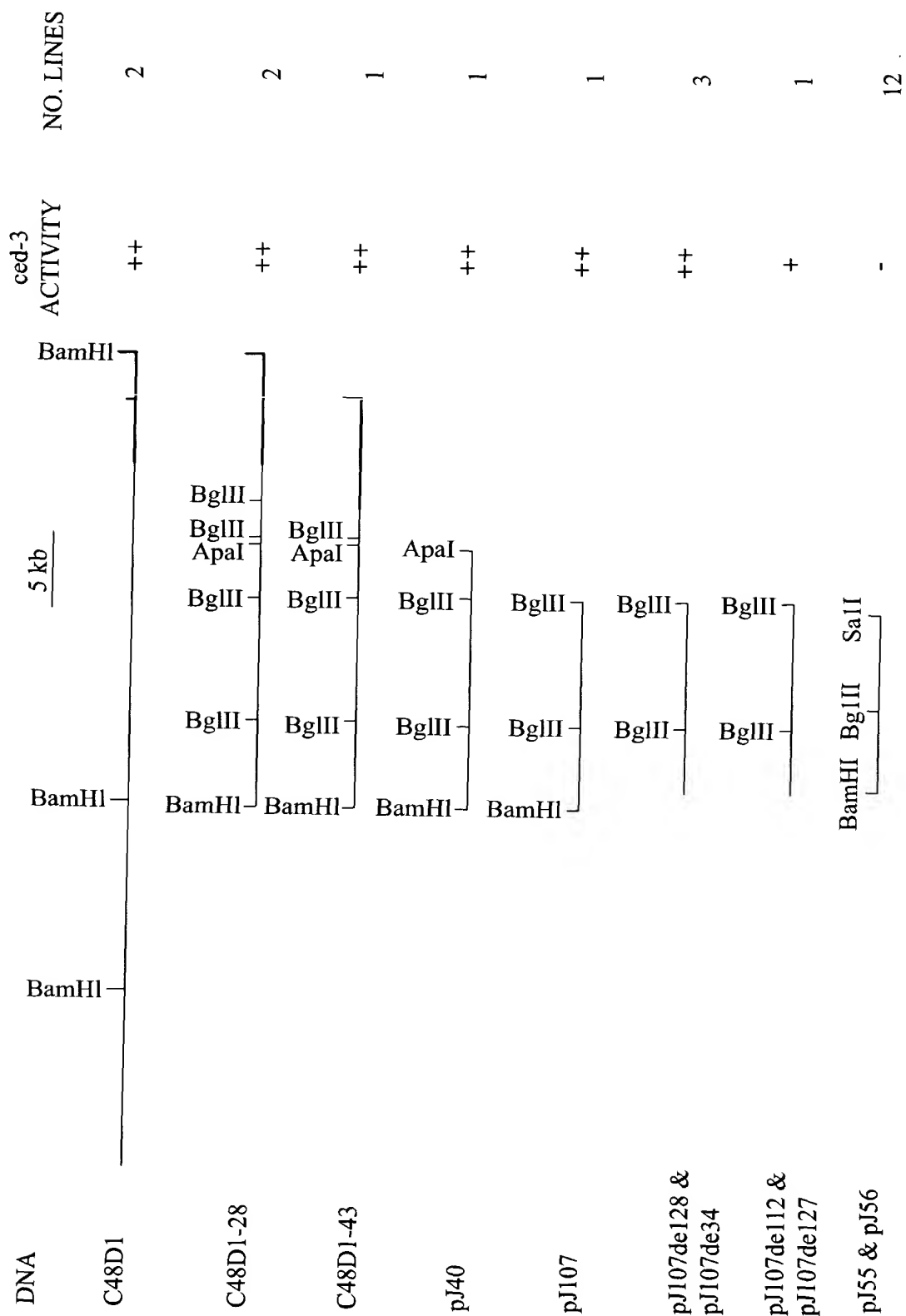


Fig. 2

ced-3 Genomic Sequence

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AGATCTGAAATAAGGTGATAAATTAATAAATTAAGTGTATTTCTGAGGAAATTTGACTGT
1  -----+-----+-----+-----+-----+-----+ 60
TTTAGCACAATTAATCTTGTTCAGAAAAAAGTCCAGTTTCTAGATTTTCCGTCTTA
61  -----+-----+-----+-----+-----+-----+ 120
TTGTCTGAATTAATATCCCTATTATCACTTTTTCATGCTCATCCTCGAGCGGCACGTCCTC
121 -----+-----+-----+-----+-----+-----+ 180
AAAGAATTGTGAGAGCAAACGCGCTCCCATTGACCTCCACACTCAGCCGCCAAAACAAAC
181 -----+-----+-----+-----+-----+-----+ 240
GTTCTGAACATTTCGTGTGTTGTGCTCCTTTTCCGTTATCTTGCAGTCATCTTTTGTCTT
241 -----+-----+-----+-----+-----+-----+ 300
TTTTCTTTGTTCTTTTGTGAACGTGTTGCTAAGCAATTATTACATCAATTGAAGAAAA
301 -----+-----+-----+-----+-----+-----+ 360
GGCTCGCCGATTTATTGTTGCCAGAAAGATTCTGAGATTCTCGAAGTCGATTTTATAATA
361 -----+-----+-----+-----+-----+-----+ 420
TTTAACCTTGGTTTTTGCATTGTTTCGTTTAAAAAAACCACTGTTTATGTGAAAAACGA
421 -----+-----+-----+-----+-----+-----+ 480
TAGTTTACTAATAAAACTACTTTTAAACCTTTACCTTTACCTCACCGCTCCGTGTTTCATG
481 -----+-----+-----+-----+-----+-----+ 540
GCTCATAGATTTTCGATACTCAAATCCAAAAATAAATTTACGAGGGCAATTAATGTGAAA
541 -----+-----+-----+-----+-----+-----+ 600
CAAAAACAATCCTAAGATTCCACATGTTTGACCTCTCCGGCACCTTCTTCTTAGCCCC
601 -----+-----+-----+-----+-----+-----+ 660
ACCACTCCATCACCTCTTTGGCGGTGTTCTTCGAAACCCACTTAGGAAAGCAGTGTGTAT
661 -----+-----+-----+-----+-----+-----+ 720
CTCATTTGGTATGCTCTTTTCGATTTTATAGCTCTTTGTGCAATTTCAATGCTTTAAAC
721 -----+-----+-----+-----+-----+-----+ 760
AATCCAAATCGCATTATATTTGTGCATGGAGGCAAATGACGGGGTTGGAATCTTAGATGA
781 -----+-----+-----+-----+-----+-----+ 840
GATCAGGAGCTTTCAGGGTAAACGCCCCGGTTCATTTTGTACCACATTTTCATCATTTTCTT
841 -----+-----+-----+-----+-----+-----+ 900
GTCGTCCTTGGTATCCTCAACTTGTCCCGGTTTTGTTTTTCGGTACACTCTTCCGTGATGC
901 -----+-----+-----+-----+-----+-----+ 960
CACCTGTCTCCGTCTCAATTATCGTTTAAATGTGAAGTGTCCAGATGGGTGACTCATA
961 -----+-----+-----+-----+-----+-----+ 1020
TTGCTGCTGCTACAATCCACTTTCTTTTCTCATCGGCAGTCTTACGAGCCCATCATAAAC
1021 -----+-----+-----+-----+-----+-----+ 1080
TTTTTTTTCCGCGAAATTTGCAATAAACCGGCCAAAAACTTTCTCCAAATTGTTACGCAA
1081 -----+-----+-----+-----+-----+-----+ 1140
TATATACAATCCATAAGAATATCTTCTCAATGTTTATGATTCTTCGCAGCACTTTCTCT
1141 -----+-----+-----+-----+-----+-----+ 1200
TCGTGTGCTAACATCTTATTTTATAATATTTCCGCTAAAAATCCGATTTTGTAGTATTA
1201 -----+-----+-----+-----+-----+-----+ 1260
ATTTATCGTAAAATTATCATAATAGCACCGAAAACACTAAAAATGGTAAAAGCTCCTTT
1261 -----+-----+-----+-----+-----+-----+ 1320

                                     Repeat 1
                                     =====
TAAATCGGCTCGACATTATCGTATTAAGGAATCACAAAATCTGAGAATGCGTACTGCGC
1321 -----+-----+-----+-----+-----+-----+ 1380

=====
AACATATTTGACGGCAAAATATCTCGTAGCGAAAACACTACAGTAATCTTTAAATGACTAC
1381 -----+-----+-----+-----+-----+-----+ 1440

```

Fig. 3

Repeat 1

```

=====>
1441 TGTAGCGCTTGTGTCGATTACGGGCTCAATTTTGGAAAATAATTTTTTTTTTCGAATTT 1500
-----+-----+-----+-----+-----+-----+-----+
=====
1501 TGATAACCCGTAAATCGTCACAACGCTACAGTAGTCATTTARAGGATTACTGTAGTTCTA 1560
-----+-----+-----+-----+-----+-----+-----+
1561 GCTACGAGATATTTTGC GCGCCAAATATGACTGTAATACGCATTCTCTGAATTTTGTGTT 1620
-----+-----+-----+-----+-----+-----+-----+
1621 TCCGTAATAATTTTCAACAAGATTTTGGCATTCCACTTTTAAAGGCGCACAGGATTTATTCCA 1680
-----+-----+-----+-----+-----+-----+-----+
1681 ATGGGTCTCGGCACGCAAAAAGTTTGATAGACTTTTAAATTCTCCTTGCATTTTAAATTC 1740
-----+-----+-----+-----+-----+-----+-----+
1741 AATTACTAAAATTTTCGTGAATTTTCTGTTAAAATTTTAAAATCAGTTTCTAATATT 1800
-----+-----+-----+-----+-----+-----+-----+
1801 TTCCAGGCTGACAAACAGAAACAAAACACAACAAACATTTTAAAATCAGTTTCAAAT 1860
-----+-----+-----+-----+-----+-----+-----+
1861 TAAAAATAACGATTTTCTCATTGAAAATTGTGTTTTATGTTTGCGAAAATAAAAGAGAACT 1920
-----+-----+-----+-----+-----+-----+-----+
1921 GATTCAAAACAATTTTAAACAAAAAAAACCCCAAAATTCGCCAGAAATCAAGATAAAAAA 1980
-----+-----+-----+-----+-----+-----+-----+
1981 TTCAAGAGGGTCAAATTTTCCGATTTTACTGACTTTCACCTTTTTTTTCGTAGTTCAGT 2040
-----+-----+-----+-----+-----+-----+-----+
2041 GCAGTTGTTGGAGTTTTTGGACGAAACTAGGAAAAAATCGATAAAAATTACTCAAATCG 2100
-----+-----+-----+-----+-----+-----+-----+
2101 AGCTGAATTTTGAGGACAATGTTTAAAAAAAACACTATTTTCCAATAATTTCACTCAT 2160
-----+-----+-----+-----+-----+-----+-----+

-----
TTTCAGACTAAATCGAAAATCAAATCGTACTCTGACTACGGGTCAGTAGAGAGGTCAACC
-----

2161 -----+-----+-----+-----+-----+-----+-----+ 2220
2221 ATCAGCCGAAGATGATGCGTCAAGATAGAAGGAGCTTGCTAGAGAGGAACATTATGATGT 2280
-----+-----+-----+-----+-----+-----+-----+
          M M R Q D R R S L L E R N I M M F
          1                                10

                                T (nl040)
                                |
2281 TCTCTAGTCATCTAAAAGTCGATGAAATTCTCGAAGTTCTCATCGCAAAACAAGTGTGTA 2340
-----+-----+-----+-----+-----+-----+-----+
          S S H L K V D E I L E V L I A K Q V L N
          20                                30

                                |intron 1
2341 ATAGTGATAATGGAGATATGATTAATGTGAGTTTTTAATCGAATAATAATTTTAAAAAAA 2400
-----+-----+-----+-----+-----+-----+-----+
          S D N G D M I N
          40

                                |
2401 AATTGATAATATAAGAATATTTTGCAGTCATGTGGAACGGTTCGCGAGAAGAGACGGG 2460
-----+-----+-----+-----+-----+-----+-----+
                                S C G T V R E K R R E
                                50

```

Fig. 3 (cont.)

5/24
A(n718)

AGATCGTGAAAGCAGTGCAACGACGGGAGATGTGGCGTTCGACGCGTTTTATGATGCTC
2461 -----+-----+-----+-----+-----+ 2520
I V K A V Q R R G D V A F D A F Y D A L
60 70

| intron 2

TTCGCTCTACGGGACACGAAGGACTTGCTGAAGTTCTTGAACCTCTCGCCAGATCGTAGG
2521 -----+-----+-----+-----+-----+ 2580
R S T G H E G L A E V L E P L A R S
80 90

TTTTTAAAGTTCGGCGCAAAAGCAAGGGTCTCACGGAAAAAAGAGGCGGATCGTAATTTT
2581 -----+-----+-----+-----+-----+ 2640
GCAACCCACCGGCACGGTTTTTTTCTCCGAAAATCGGAAATTATGCACTTTCCCAAATAT
2641 -----+-----+-----+-----+-----+ 2700
TTGAAGTGAAATATATTTTATTTACTGAAAGCTCGAGTGATTATTTATTTTAAACACTA
2701 -----+-----+-----+-----+-----+ 2760
ATTTTCGTGGCGCAAAAGGCCATTTTGTAGATTGCGGAAAATACTTGTCACACACACAC
2761 -----+-----+-----+-----+-----+ 2820

|

ACACACATCTCCTTCAAATATCCCTTTTCCAGTGTGACTCGAATGCTGTCGAATTCGA
2821 -----+-----+-----+-----+-----+ 2880
V D S N A V E F E
100

GTGTCCAATGTCACCGGCAAGCCATCGTCGGAGCCGCGCATTGAGCCCCGCCGGCTACAC
2881 -----+-----+-----+-----+-----+ 2940
C P M S P A S H R R S R A L S P A G Y T
110 120

TTCACCGACCCGAGTTCACCGTGACAGCGTCTCTTCAGTGTGTCATTCATTCTTATCA
2941 -----+-----+-----+-----+-----+ 3000
S P T R V H R D S V S S V S S F T S Y Q
130 140

GGATATCTACTCAAGAGCAAGATCTCGTTCTCGATCGCGTGCACTTCATTCATCGGATCG
3001 -----+-----+-----+-----+-----+ 3060
D I Y S R A R S R S R S R A L H S S D R
150 1 60

| intron 3

ACACAATTATTCATCTCCTCCAGTCAACGCATTTCCAGCCAACCTTGATGTTGATGCG
3061 -----+-----+-----+-----+-----+ 3120
H N Y S S P P V N A F P S Q P S
170

Repeat 1

=====

AACACTAAATTCTGAGAATGCGCATTACTCAACATATTTGACGCGCAAATATCTCGTAGC
3121 -----+-----+-----+-----+-----+ 3180

=====

GAAAAATACAGTAACCCTTTAAATGACTATTGTAGTGTGATTTACGGGCTCGATTTTCG
3181 -----+-----+-----+-----+-----+ 3240

Fig. 3 (cont.)

6/24

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==>
3241 AAACGAATATATGCTCGAATTGTGACAACGAATTTTAATTTGTCATTTTTGTGTTTTCTT 3300
-----+-----+-----+-----+-----+-----+-----+

Repeat 1
<=====
3301 TTGATATTTTTGATCAATTAATAAATTATTTCCGTAAACAGACACCAGCGCTACAGTACT 3360
-----+-----+-----+-----+-----+-----+-----+

=====
3361 CTTTTAAAGAGTTACAGTAGTTTTTCGCTTCAAGATATTTTGAAAAGAATTTTAAACATTT 3420
-----+-----+-----+-----+-----+-----+-----+
3421 TGAAAAAAAATCATCTAACATGTGCCAAAACGCTTTTTTCAAGTTTCGCAGATTTTTTTGA 3480
-----+-----+-----+-----+-----+-----+-----+

Repeat 2
=====
3481 TTTTTTTCATTCAAGATATGCTTATTAACACATATAATTATCATTAAATGTGAATTTCTTG 3540
-----+-----+-----+-----+-----+-----+-----+

=====
3541 TAGAAATTTTGGGCTTTTCGTTCTAGTATGCTCTACTTTTGAAATTGCTCAACGAAAAAA 3600
-----+-----+-----+-----+-----+-----+-----+

=====
3601 TCATGTGGTTTGTTTCATATGAATGACGAAAAATAGCAATTTTTTATATATTTTCCCCTAT 3660
-----+-----+-----+-----+-----+-----+-----+

=====
3661 TCATGTTGTGCAGAAAAATAGTAAAAAAGCGCATGCATTTTTTCGACATTTTTTACATCGA 3720
-----+-----+-----+-----+-----+-----+-----+

=====>
3721 ACGACAGCTCACTTCACATGCTGAAGACGAGAGACGCGGAGAAATACCACACATCTTTCT 3780
-----+-----+-----+-----+-----+-----+-----+

Repeat 2
<=====
3781 GCGTCTCTCGTCTTCAGCATGTGAAATGGGATCTCGGTGATGTAAAAAATGTCAATA 3840
-----+-----+-----+-----+-----+-----+-----+

=====
3841 ATGTAAAAAATGCATGCGTTTTTTTTACACTTTTCTGCACAAATGAATAGGGGGAAAATGT 3900
-----+-----+-----+-----+-----+-----+-----+

=====
3901 ATTAAAATACATTTTTTTGTATTTTTCAACATCACATGATTAACCCCATTTTTTTTCGTT 3960
-----+-----+-----+-----+-----+-----+-----+

=====
3961 GAGCAACTTAAAAAGTAGAGAATATTAGAGCGAAAACCAAATTTCTTCAAGATATTACC 4020
-----+-----+-----+-----+-----+-----+-----+

=====
4021 TTTATTGATAATTATAGATGTTAATAAGCATATCTTGAATGAAAGTCAGCAAAAATATGT 4080
-----+-----+-----+-----+-----+-----+-----+

```

Fig. 3 (cont.)

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4081 -----+-----+-----+-----+-----+-----+ 4140
 TTTTTCGATTTTCTACATCACATGAATGTAGAAAATTAAAAGGGAAATCAAAATTTCTA
 4141 -----+-----+-----+-----+-----+-----+ 4200
 GAGGATATAATTGAATGAAACATTGCGAAATTAAAATGTGCGAAACGTCAAAAAAGAGGA
 4201 -----+-----+-----+-----+-----+-----+ 4260

 AATTTGGGTATCAAAATCGATCCTAAAACCAACACATTTTCAGCATCCGCCAACTCTTCAT
 4261 -----+-----+-----+-----+-----+-----+ 4320
 S A N S S F
 180
 TCACCGGATGCTCTTCTCTCGGATACAGTTCAAGTCGTAATCGCTCATTTCAGCAAAGCTT
 4321 -----+-----+-----+-----+-----+-----+ 4380
 T G C S S L G Y S S S R N R S F S K A S
 190 200
 CTGGACCAACTCAATACATATTCATGAAGAGGATATGAACTTTGTCGATGCACCAACCA
 4381 -----+-----+-----+-----+-----+-----+ 4440
 G P T Q Y I F H E E D M N F V D A P T I
 210 220
 TAAGCCGTGTTTTTCGACGAGAAAACCATGTACAGAACTTCTCGAGTCCTCGTGGAATGT
 4441 -----+-----+-----+-----+-----+-----+ 4500
 S R V F D E K T M Y R N F S S P R G M C
 230 240
 GCCTCATCATAAATAATGAACACTTTGAGCAGATGCCAACACGGAATGGTACCAAGGCCG
 4501 -----+-----+-----+-----+-----+-----+ 4560
 L I I N N E H F E Q M P T R N G T K A D
 250 260
 ACAAGGACAATCTTACCAATTTGTTTCAGATGCATGGGCTATACGGTTATTTGCAAGGACA
 4561 -----+-----+-----+-----+-----+-----+ 4620
 K D N L T N L F R C M G Y T V I C K D N
 270 280
 | intron 4
 ATCTGACGGGAAGGGTACGGCGAAATTATATTACCCAAACGCGAAATTTGCCATTTTGCG
 4621 -----+-----+-----+-----+-----+-----+ 4680
 L T G R

 Repeat 3
 =====>
 CCGAAAATGTGGCGCCCGGTCTCGACACGACAATTTGTGTTAAATGCAAAAATGTATAAT
 4681 -----+-----+-----+-----+-----+-----+ 4740
 TTTGCAAAAACAAAATTTTGAAGTTCCGCGAAAATGATTTACCTAGTTTCGAAATTTTC
 4741 -----+-----+-----+-----+-----+-----+ 4800
 GTTTTTTCCGGCTACATTATGTGTTTTTTCTTAGTTTTTCTATAATATTTGATGTAAAAA
 4801 -----+-----+-----+-----+-----+-----+ 4860
 ACCGTTTGTAATTTTCAGACAATTTCCGCATACAAAACCTTGATAGCACGAAATCAATT
 4861 -----+-----+-----+-----+-----+-----+ 4920
 TTCTGAATTTTCAAAATTATCCAAAATGCACAATTTAAAATTTGTGAAAATTGGCAAAC
 4921 -----+-----+-----+-----+-----+-----+ 4980

Fig. 3 (cont.)

8/24

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GGTGTTC AATATGAAATGTATTTTTTAAAACTTTAAAAACCACTCCGGAAGCAATAA
4981 -----+-----+-----+-----+-----+-----+ 5040
AAATCAAAACAACGTCACAATTCAAATTCAAAAGTTATTCATCCGATTTGTTTATTTTTG
5041 -----+-----+-----+-----+-----+-----+ 5100
CAAAATTTGAAAAAATCATGAAGGATTTAGAAAAGTTTATAACATTTTTTCTAGATTTT
5101 -----+-----+-----+-----+-----+-----+ 5160
TCAAAATTTTTTTTAAACAAATCGAGAAAAAGAGAATGAAAAATCGATTTTAAAAATATCC
5161 -----+-----+-----+-----+-----+-----+ 5220

Repeat 3
<=====
ACAGCTTCGAGAGTTTGAAATTACAGTACTCCTTAAAGGCGCACACCCCATTTGCATTGG
5221 -----+-----+-----+-----+-----+-----+ 5280

=====
ACCAAAAAATTTGTCGTGTCGAGACCAGGTACCGTAGTTTTTGTGCGAAAAATTCACCAT
5281 -----+-----+-----+-----+-----+-----+ 5340
TGGACAATAAACCTTCCTAATCACCAAAAAGTAAAATTGAAATCTTCGAAAAGCCAAAAA
5341 -----+-----+-----+-----+-----+-----+ 5400
ATTCAAAAAAAAAGTCGAATTTTCGATTTTTTTTTTTGGTTTTTTGGTCCCAAAACCAAAA
5401 -----+-----+-----+-----+-----+-----+ 5460
AAATCAATTTTCTGCAAAATACCAAAAAGAAACCCGAAAAAATTTCCCAGCCTTGTTCTT
5461 -----+-----+-----+-----+-----+-----+ 5520

AATGTAAACTGATATTTAATTTCCAGGGAATGCTCCTGACAATTCGAGACTTTGCCAAAC
5521 -----+-----+-----+-----+-----+-----+ 5580
                        G M L L T I R D F A K H
                        290                        300

ACGAATCACACGGAGATTCTGCGATACTCGTGATTCTATCACACGGAGAAGAGAATGTGA
5581 -----+-----+-----+-----+-----+-----+ 5640
    E S H G D S A I L V I L S H G E E N V I
                        310                        320
TTATTGGAGTTGATGATATACCGATTAGTACACACGAGATATATGATCTTCTCAACGCGG
5641 -----+-----+-----+-----+-----+-----+
    I G V D D I P I S T H E I Y D L L N A A
                        330                        340

                                                A(n2433)
                                                | |
CAAATGCTCCCCGTCTGGCGAATAAGCCGAAAATCGTTTTTGTGCAGGCTTGTCGAGGCG
5701 -----+-----+-----+-----+-----+-----+ 5760
    N A P R L A N K P K I V F V Q A C R G E
                        350                        360

                                                |
GTTTCGTTTTTTATTTTAATTTTAATATAAATATTTTAAATAAATTCATTTTCAGAACGTC
5761 -----+-----+-----+-----+-----+-----+ 5820
                                                R R

GTGACAATGGATTCCCAGTCTTGATTCTGTGCGACGGAGTTCCTGCATTTCTTCGTCGTG
5821 -----+-----+-----+-----+-----+-----+ 5880
    D N G F P V L D S V D G V P A F L R R G
                        370                        380

```

Fig. 3 (cont.)

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Fig. 3 (cont.)

10/24

Repeat 5

```

=====
CTTGAAACAAACAATGCATGTCTAACTTTTAAGGACACAGAAAAATAGGCAGAGGCTCCT
6541 -----+-----+-----+-----+-----+-----+ 6600

=====>
TTTGCAAGCCTGCCGCGCGTCAACCTAGAATTTTAGTTTTAGCTAAAATGATTGATTTT
6601 -----+-----+-----+-----+-----+-----+ 6660
GAATATTTTATGCTAATTTTTTTGCGTTAAATTTTGAAATAGTCACTATTTATCGGGTTT
6661 -----+-----+-----+-----+-----+-----+ 6720
CCAGTAAAAAATGTTTATTAGCCATTGGATTTTACTGAAAACGAAAATTTGTAGTTTTTC
6721 -----+-----+-----+-----+-----+-----+ 6780
AACGAAATTTATCGATTTTTTAAATGTAAAAAATAAGCGAAAATTACATCAACCATCAA
6781 -----+-----+-----+-----+-----+-----+ 6840
GCATTTAAGCCAAAATTGTTAACTCATTTAAAAATTAATTCAAAGTTGTCCACGAGTATT
6841 -----+-----+-----+-----+-----+-----+ 6900

```

Repeat 5

```

<=====
ACACGGTTGGCGCGCGGCAAGTTTGCAAACGACGCTCCGCCTCTTTTTCTGTGCGGCTT
6901 -----+-----+-----+-----+-----+-----+ 6960

=====
GAAAACAAGGGATCGGTTTAGATTTTTCCCAAATTTAAATTAAATTCAGATGACATC
6961 -----+-----+-----+-----+-----+-----+ 7020
                                     M T S

CCGCCTGCTCAAAAAGTTCTACTTTTTGGCCGGAAGCACGAAACTCTGCCGTCTAAAATTC
7021 -----+-----+-----+-----+-----+-----+ 7080
  R L L K K F Y F W P E A R N S A V *
          490                      500

ACTCGTGATTCATTGCCCAATTGATAATTGTCTGTATCTTCTCCCCCAGTTCTCTTTCGC
7081 -----+-----+-----+-----+-----+-----+ 7140
CCAATTAGTTTAAAACCATGTGTATATTGTTATCCTATACTCATTTCACTTTATCATTCT
7141 -----+-----+-----+-----+-----+-----+ 7200
ATCATTTCTCTTCCCATTTTCACACATTTCCATTTCTCTACGATAATCTAAAATTATGAC
7201 -----+-----+-----+-----+-----+-----+ 7260
GTTTGTGTCTCGAACGCATAATAATTTAATAACTCGTTTTGAATTTGATTAGTTGTTGT
7261 -----+-----+-----+-----+-----+-----+ 7320
GCCCAGTATATATGTATGTACTATGCTTCTATCAACAAAATAGTTTCATAGATCATCACC
7321 -----+-----+-----+-----+-----+-----+ 7380
CCAACCCACCAACCTACCGTACCATATTCAATTTTGGCCGGAATCAATTTTCGATTAATT
7381 -----+-----+-----+-----+-----+-----+ 7440
TTAACCTATTTTTTCGCCACAAAAAATCTAATATTTGAATTAACGAATAGCATTCCCATC
7441 -----+-----+-----+-----+-----+-----+ 7500
TCTCCCGTGCCGGAATGCCTCCCGGCCTTTTAAAGTTTCGGAACATTTGGCAATTATGTAT
7501 -----+-----+-----+-----+-----+-----+ 7560
AAATTTGTAGGTCCCCCCCATCATTTCCCGCCCATCATCTCAAATTGCATTCTTTTTTCG
7561 -----+-----+-----+-----+-----+-----+ 7620
CCGTGATATCCCGATTCTGGTCAGCAAAGATCT
7621 -----+-----+-----+-----+-----+ 7653

```

Fig. 3 (cont.)

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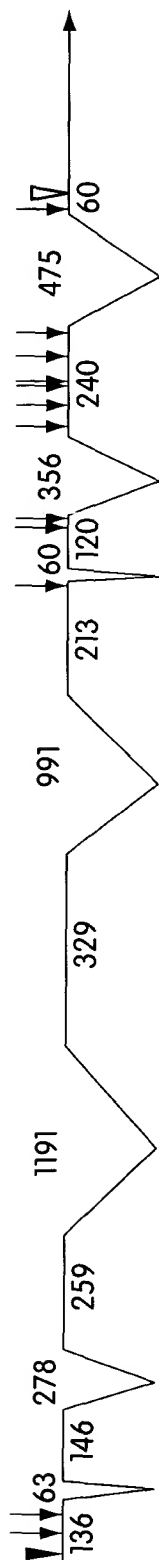


Fig. 4A

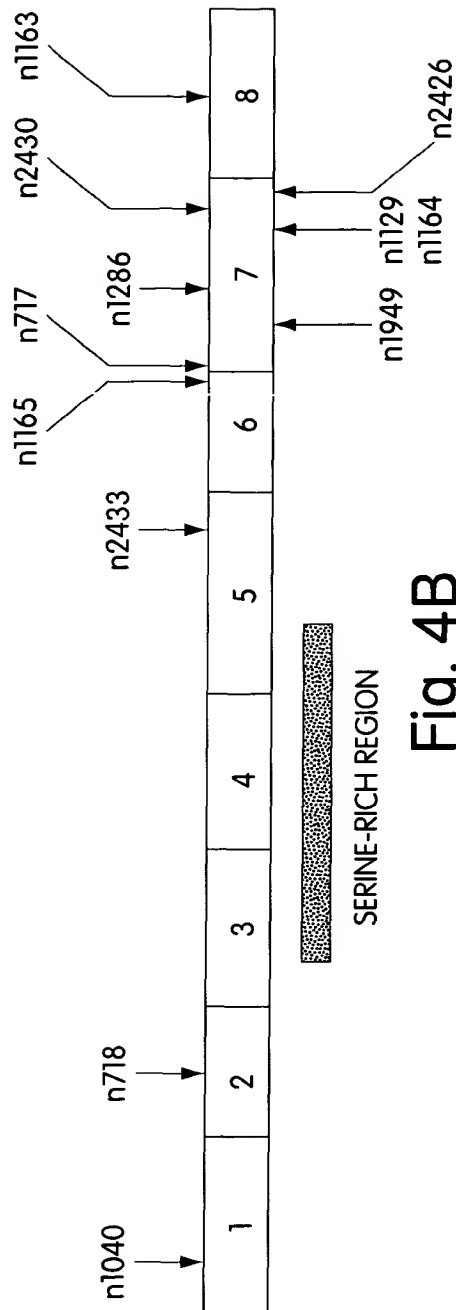


Fig. 4B

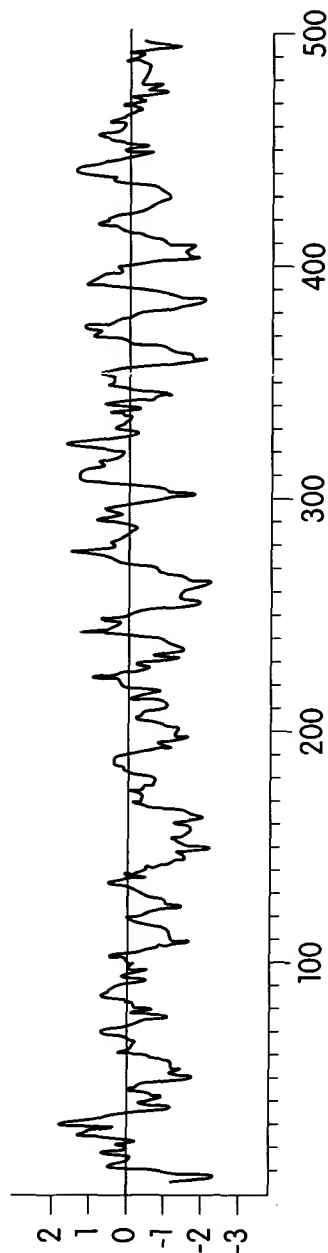


Fig. 5

12/24

Alignment of ced-3 and Human Interleukin -1 β convertase

ICE	1	MADKVLKEKRKLFIRSM....GEGTINGLLDELLQTRVLNKEEMEKVKRE
		: : : : : : : : : : : : : : : : : .
Ced-3	1	...MMRQDRRSLLERNIMMFSSHLKVDEILEVLIQVLNSDNGDMIN.S
		↓ F
BGAfQ		=====
PBA		=====
	47	NATVMDKTRALIDSVIPKGAQACQ.ICITYICEEDSYLAGTLGLSADQTS
		: : : : : : : : : : : : : : : .
	47	CGTVREKRREIVKAVQRPQDVAFDAFYDALRSTGHEGLAEVLEPLARSVD
		↓ R
BFAfQ		=====
PBA		=====
	96	GNYLNMQ.....autocleavage site.....DSQGVLSFF.....
		: : : : : : : : : : : : :
	97	<u>SNAVEFECPMSPASHRRSRALSPAGYTSPTVRHRDSVSSVSSFTSYODIY</u>
		serine-rich region
BGAfQ		=====
PBA		=====
	112PAPQAVQDNPAMPTSSGSEGNVKLCSLE
		: : : : : : : : : : : : : .
	147	<u>SRARSRSRSLHSSDRHNYSSPPVNAFPSOPSSANSSTGCSSLGYSS</u>
BGAfQ		=====
PBA		===
	140	EAQRIWKQKSAEIYPIMDK.....SSRTRLAL
		: : : : : : : : : : : : : : : : : : : :
	197	<u>RNRSFSKASGPTQYIFHEEDMNFVDAPTISR VFDEKTM YRNFS SPRGMCL</u>
BGAfQ		=====

Fig. 6A

0988243-062201

```

217 AFAHRPEHKTS DSTFLVFM SHGIREGICGKKHSEQVPDI.LQLNAIFNML
    .|||...| :|||.:||:|||| :.|| |.| |.:|::|
297 DFAKHESH..GDSAILVILSHGEENVIIG.....VDDIPISTHEIYDLL

BGAFAQ =====
```

```

315 DDAI.....KKAHIEKDFAFCSSTPDNVSWRHPTMGSVFI
    ::          :| . : |:: ..|:: ||||:..|| ||
389 GPLFNFLGCVRPQVQQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFI
      ↓                ↓
     stop             stop

```

```

395   TRCFYLFPGH*.... 404
      : ||::|:
489   LKKFYFWPEARNSAV 503

```

Fig. 6A (cont.)

Alignment of Ced-3 and Murine NEDD-2

```

Ced-3   251  EHFEQMPTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRCMLLTIRDFAK  300
NEDD-2   1  .....:|:|.
          9  .....MLTVQVYRT
          301 HESHGDSAILVILSHGENVIIGVDDIPISTHEIYDLLNAANAPRLANKP  350
          10  SOKCSSSKHV.....EVLLD....PLGT.SFCSLL.....PP  37
          351 KIVFVQACRGERRDNGFPVLDSDVGVPFLRRGWDNRDGPLNFLGCVRP  400
          38  PLLLYETDRGVDDQDGKNHTQSPGC.....EESDAGKEELM.....  73
          401  QVQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFIQAVCEVFSTHAK  450
          74  ....KMRLPTRSDMICGYACLKGNAAAMRNTKRGSWYIEALTQVFSERAC  118
              n2426 K  F n1163
          451  DMDVVELLTEVNK..KVACGFQTSQGSNLIKQMPENTSRLLKKFYFWPEA  498
          119  DMHVADMLVKVNALIKEREGYAPGTEFHRCKEMSEYCSLTCQQLYLPFGY  168

          499  RNSAV  503
          169  PPT... 172

```

Fig. 6B

Alignment of N-terminal regions of ced-3/ICE- related proteins

c. briggsae ced-3	MMRQDRWSLLERNILEFSSKLQADLILDVLIQVLSNDGVDVNSCRTERDNEKEIVKAVQRRGDEAFDAFYDALRDTGHNDLADVLMPLSR---PNPV	
ced-3 protein	MMRQDRWSLLERNIMFSSHLKVDLEVLIAQVLSNDGMDINSCGTVRKREIVKAVQPCGVAFDAFYDALRSTGHEGLAEVLEPLARSVDNAV 100	
C. vulgaris ced-3	-----	
Mouse ICE.gw	M-----ADKIL-----RAKKQFINSV---SIGTINGLLDELLEK-----RVLNQDEEM---DKI	
Human ICE.GW	M-----ADKVL-----KEKKLFIRSM---GEGTINGLLDELLQT-----RVLNKEEM---EKV	
Consensus	M.....AD.IL.....V...G.....D.L..T.....VL.....V	
c. briggsae ced-3	PMCEPMSPPSHRRSRALSPPGYASPTRVHRDSTISSVSFTSTVDVYSRRSSSRSLQSSDRHNYMSAA-TSPSPQSSANSFTGCASLGYSSSRN	
ced-3 protein	EPECMPSPASHRRSRALSPAGYTSPTVRHRDSTSSVSFTSYQD-IYSRRSRSS-RALHSSDRHNYSPPVNAFPQSPSSANSFTGCSSLGYSSSRN 198	
C. vulgaris ced-3	-----STSRSSRPLETSDRHNYSVPS-NSFQSQPASANSFTGSSSLGYSSSRT	
Mouse ICE.gw	KLA---NITAMDKARDLCDHVSXKGPQASQIFTYICNEDCYL-----AGILEQSAPSAE--TFVAT-----EDSKGGHPSSETKEEQNKED-G	
Human ICE.GW	KRE---NATVMDKTRALIDSVIPGAQACQICITYICEEDSYL-----AGTIGLSADQTSQ--NYLNM-----QDSQGVLSSEFPAPQAVQNDPAMP	
Consensus	..E-----RAL.....I.....SY.....S.SRS.R.L.SSDRHY.S...-..F.SQP.SANSFTG.-SLGYSSSR.	
c. briggsae ced-3	RSFSKTSAQSYIFHEEDMNYVDAPTIHRVFDEKTYRNFSSPRGLCLIIINNEHFEQMPTRNGTKAKDKNLTNIFRCMGYTVI CKDNLITGREMLSTIRSF	
ced-3 protein	RSFSKASGPTQYIFHEEDMNFVDAPTISRVFDEKTYRNFSSPRGNCGLIINNEHFEQMPTRNGTKAKDKNLTNLFCMGYTVI CKDNLITGRGMLLTIRDF	
C. vulgaris ced-3	RSYSKASAHSQYIFHEEDMNYVDAPTIHRVFDEKTYRNFSTPRGLCLIIINNEHFEQMPTRNGTKAFKDKNISNLFCMGYTVI CKDNLITGRMML-TIRDF	
Mouse ICE.gw	TFPGLTGTLKFCPLEKAQKLWKENPS--EIIY--PIMNTT-TRTR-LALII CNTFFQHLSPRVGAQVDLREMKLLLEDLGYTVKVKENLTALENVKEVKEF	
Human ICE.GW	TSSGSEGNVKLCSLEEAQRIWKQKSA--EIIY--PIMDKS-SRTR-LALII IONEEDTSIPRRITGAEVDTTGMTWLLQNLGYSVDVKKNLTA S DMTTELEAF	
Consensus	RS.SK.S...QYIFHEEDMN.VDAPTI.RVFDEKTYRNFSSPRGLCLIIINNEHFEQMPTRNGTK.DKDN.TNLFCMGYTVI.CKDNLITGR.ML.TIR.F	
c. briggsae ced-3	GRNDME--GDSA ILVTLSHGEENVIIIG---VDDVS--VNVHEITVDLINAANAAPRLANKPKL VVVQACRG	
ced-3 protein	AKHESH--GDSA ILVTLSHGEENVIIIG---VDDIP--ISTHEITVDLINAANAAPRLANKPKI VVVQACRG	
C. vulgaris ced-3	AKNETH--GDSA ILVTLSHGEENVIIIG---VDDVS--VNVHEITVDLINAANAAPRLANKPKL VVVQACRG	
Mouse ICE.gw	AACPHEKTS DSTFLVFM SHGIQEGICGTTYSNEVSDILKVDITFQMMNTLNCPSLKDKPKVII IQACRG	
Human ICE.GW	AHRPEKTS DSTFLVFM SHGIRREGICGKKHSEQVPDILQLNALFNMLNTKNCPSLKDKPKVII IQACRG	
Consensus	A.....H...CDSA ILVTLSHGEENVIIIG---VDDVS---VHEITVDLINAANAAPRLANKPKL VVVQACRG	

Fig. 6C

Alignment of C-terminal regions of ced-3/ICE/NEDD-2 - related proteins

ICE C-terminus	DSPGVW---	-----	--FKDSVG--	-----	-----V
Mouse ICE C-ter	EKGQVL---	-----	--LKDSVR--	-----	-----D
C. briggsae C-ter	ERRDNGFP--	-----	-----	-----VPSLI	-----RRGWDN
ced-3 C-terminus	ERRDNGFP--	-----	-----	-----VPSLI	-----RRGWDN 386
C. vulgaris C-terminus	ERRDVGFP--	-----	-----	-----VPAFL	-----RRGWDK
nedd-2 protein.gw	MLTVQVYRTS	QKCSSSKHW	EVLLDPLGTS	FCSLLPFPLL	LYETDRGVDDQ
Consensus	E.....--	-----	--LDSV..-	-----P...	-----RG.D.
ICE C-terminus	SGNL----SLP	TTEFE---D	DAIKKA-HIE	KDFIAFCST	PDNVSWRHPT
Mouse ICE C-ter	SEE----DFL	TDAIFE---D	DGIKKA-HIE	KDFIAFCST	PDNVSWRHPT
C. briggsae C-ter	RDG-PLFNFL	GCVRPQV--Q	QVWRKK-PSQ	ADMLIAYATT	AQYVSWRNSA
ced-3 C-terminus	RDG-PLFNFL	GCVRPQV--Q	QVWRKK-PSQ	ADMLIAYATT	AQYVSWRNSA 432
C. vulgaris C-terminus	GDG-P--NFL	GCVRPQA--Q	QVWRKK-PSQ	ADILLIAYATT	AQYVSWRNSA
nedd-2 protein.gw	QDGKNHTQSP	GCEESDAGKE	ELMKRLPTR	SDMICGYACL	KGNAAMRNTK
Consensus	.DG-...-FL	GC.....--K.-P...	.D.....YA.T	...VSWEN..
ICE C-terminus	MGSVFIQRLI	EHMQEYACSC	DVEEIFRNV-	-RF-----SFE	QPDGRAQMPT
Mouse ICE C-ter	RGSLEFIQSLI	KHKKEYAWSC	DLEDIFRNV-	-RF-----SFE	QPEFRLQMPT
C. briggsae C-ter	RGSWFIQAVC	EVFSLHAKDM	DVVELLTFVN	KKVA--CGFQ	TSQGSNILKQ
ced-3 C-terminus	RGSWFIQAVC	EVFSTHAKDM	DVVELLTFVN	KKVA--CGFQ	TSQGSNILKQ 480
C. vulgaris C-terminus	RGSWFIQAVC	EVFSLHAKDM	DVVELLTFVN	KKVA--CGFQ	TSQGANILKQ
nedd-2 protein.gw	RGSWYIIEALT	QVFSEKACDM	HVADMLVNVN	ALIKEREGYA	PGTEFHRCKE
Consensus	RGS.FI.A..	EVFS..A.DM	DV.E.L..M.---GF.	...G.....K.
ICE C-terminus	T-ERVT-LTR	CFYLFPGH--	-----	-----	-----
Mouse ICE C-ter	A-DRVT-LTR	RFYLFPGH--	-----	-----	-----
C. briggsae C-ter	MPELTSRLK	KFYFWPEDRG	RNSAV	-----	-----
ced-3 C-terminus	MPENTSRLK	KFYFWPEAR-	-NSAV	503	-----
C. vulgaris C-terminus	MPELTSRLK	KFYFWPEDRN	RSSAV	-----	-----
nedd-2 protein.gw	MSEYCSILCQ	QLYLFPG---	-YPPT	-----	-----
Consensus	M.E...S.L.K	.FY..P..-	----	-----	-----

Fig. 6D

Lines

```

1  01  MMRQDRRSLLERNIMMFSSHLKVDEILEVLIQVLNSDNGDMINSCGTV  50
2      .....W_.....LE...K.QA.L..D.....V....R.E
3      TVSISLI..R.....  M.....

1  51  REKRREIVKAVQRPQDVAFDAFYDALRSTGHEGLAEVLEPLARSVDSNAV  100
2      .DNEK.....R..E.....D...ND..D..M..S.P    .P.
3

1  101  EFECPMSPASHRRSRALSPAGYTSPTRVHRDSVSSVSSFTS_YQDIYSRA  149
2      PM.....S.....P .A.....I.....T...V....
3      S

1  150  RSRSR_SRALHSSDRHNYSSPPVNAFPSQPSSANSSFTGCSSLGYSSSRN  198
2      ..S..S..P.Q.....M.AA_TS.....A.....
3      T...__..P..T.....V..S..S.Q...A.....S.....T

1  199  RSFSKASGPTQYIFHEEDMNFVDAPTISR VFDEKTM YRNFSSPRGMCLI  247
2      .....T.AQS.....Y.....H.....L...
3      ..Y....AHS.....Y.....H.....T...L...

1  248  INNEHFEQMPTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIRD  297
2      .....I.....E..S...S
3      .....P....IS.....I.H.....M.....

1  298  FAKHESHGDSAILVILSHGEENVIGVDDIPISTHEIYDLLNAANAPRLA  347
2      .GRNDM.....VSVNV.....
3      ...N.T.....VSVNV....x.....

1  348  NKPKIVFVQACRGERRDNGFPVLDSVDGVPAFLRRGWDNRDGPLFNFLGC  397
2      ....L.....SLI.....
3      ....L.....V.....LI.....KG...

1  398  VRPQVQQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFIQAVCEVFST  447
2      .....M..A.....L
3      ....A.....A.....L

1  448  HAKDMDVVELLTEVNKKVACGFQTSQGSNILKQMPEMTSRLLKKFYFWPE  497
2      .....L.....
3      .....A.....L.....

1  498  __ARN__SAV  503
2      DRG..__...
3      __D..RS...

```

Fig. 7

Interleukin-1 β convertase cDNA sequence

1 AAAAGGAGAG AAAAGCCATG GCCGACAAGG TCCTGAAGGA GAAGAGAAAG
 51 CTGTTTATCC GTTCCATGGG TGAAGGTACA ATAAATGGCT TACTGGATGA
 101 ATTATTACAG ACAAGGGTGC TGAACAAGGA AGAGATGGAG AAAGTAAAC
 151 GTGAAAATGC TACAGTTATG GATAAGACCC GAGCTTTGAT TGACTCCGTT
 201 ATTCCGAAAG GGGCACAGGC ATGCCAAATT TGCATCACAT ACATTTGTGA
 251 AGAAGACAGT TACCTGGCAG GGACGCTGGG ACTCTCAGCA GATCAAACAT
 301 CTGGAAATTA CCTTAATATG CAAGACTCTC AAGGAGTACT TTCTTCCTTT
 351 CCAGCTCCTC AGGCAGTGCA GGACAACCCA GCTATGCCCA CATCCTCAGG
 401 CTCAGAAGGG AATGTCAAGC TTTGCTCCCT AGAAGAAGCT CAAAGGATAT
 451 GGAAACAAAA GTCGGCAGAG ATTTATCCAA TAATGGACAA GTCAAGCCGC
 501 ACACGTCTTG CTCTCATTAT CTGCAATGAA GAATTTGACA GTATTCCTAG
 551 AAGAACTGGA GCTGAGGTTG ACATCACAGG CATGACAATG CTGCTACAAA
 601 ATCTGGGGTA CAGCGTAGAT GTGAAAAAAA ATCTCACTGC TTCGGACATG
 651 ACTACAGAGC TGGAGGCATT TGCACACCGC CCAGAGCACA AGACCTCTGA
 701 CAGCACGTTT CTGGTGTTCA TGTCTCATGG TATTCGGGAA GGCATTTGTG
 751 GGAAGAAACA CTCTGAGCAA GTCCCAGATA TACTACAACT CAATGCAATC
 801 TTAAACATGT TGAATACCAA GAACTGCCCA AGTTTGAAGG ACAAACCGAA
 851 GGTGATCATC ATCCAGGCCT GCCGTGGTGA CAGCCCTGGT GTGGTGTGGT
 901 TTAAAGATTC AGTAGGAGTT TCTGGAAACC TATCTTTACC AACTACAGAA
 951 GAGTTTGAGG ATGATGCTAT TAAGAAAGCC CACATAGAGA AGGATTTTAT
 1001 CGCTTTCTGC TCTTCCACAC CAGATAATGT TTCTTGGAGA CATCCCACAA
 1051 TGGGCTCTGT TTTTATTGGA AGACTCATTG AACATATGCA AGAATATGCC
 1101 TGTTCTCTGT ATGTGGAGGA AATTTTCCGC AAGGTTGAT TTTCAATTGA
 1151 GCAGCCAGAT GGTAAGAGCGC AGATGCCCAC CACTGAAAGA GTGACTTTGA
 1201 CAAGATGTTT CTACCTCTTC CCAGGACATT AAAATAAGGA AACTGTATGA
 1251 ATGTCTGCGG GCAGGAAGTG AAGAGATCGT TCTGTAAAAG GTTTTTTGAA
 1301 TTATGTCTGC TGAATAATAA ACTTTTTTTT AAATAATAAA TCTGGTAGAA
 1351 AAATGAAAAA AAAAAAAAAA AAA

Fig. 8

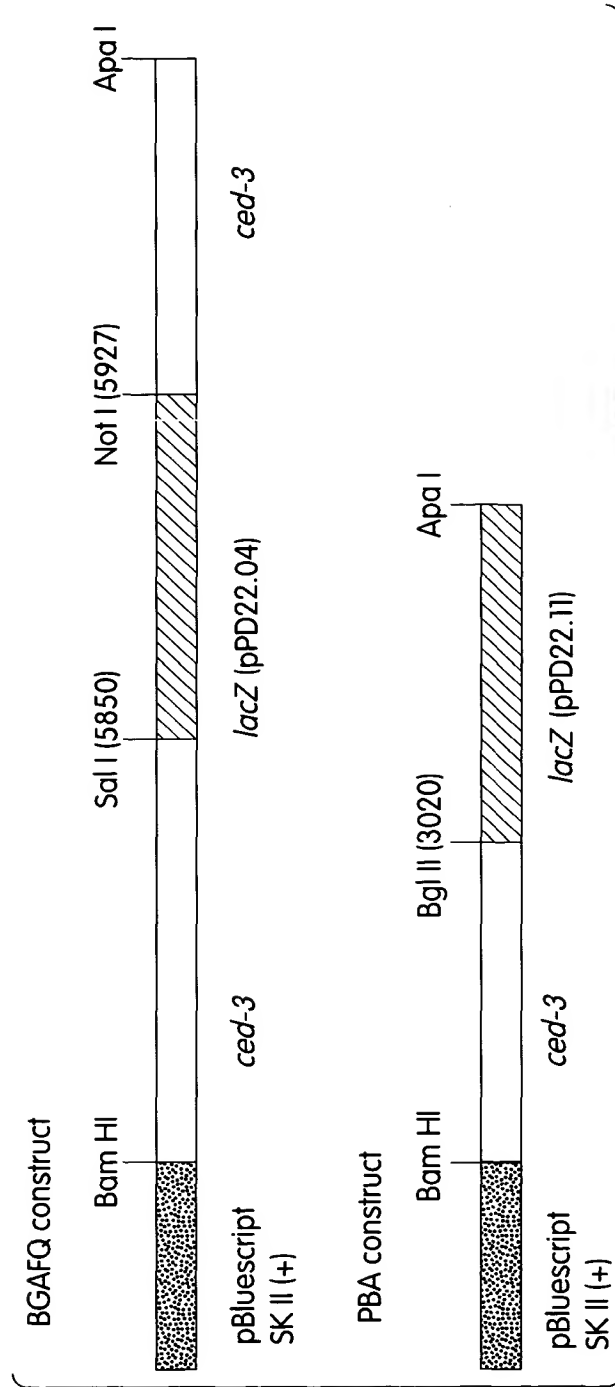


Fig.9A

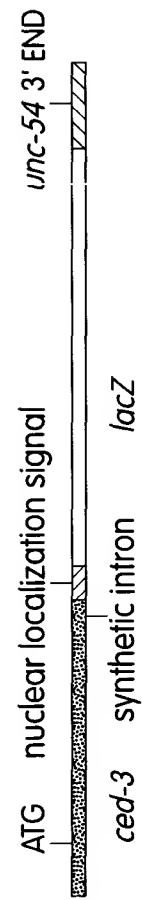


Fig.9B

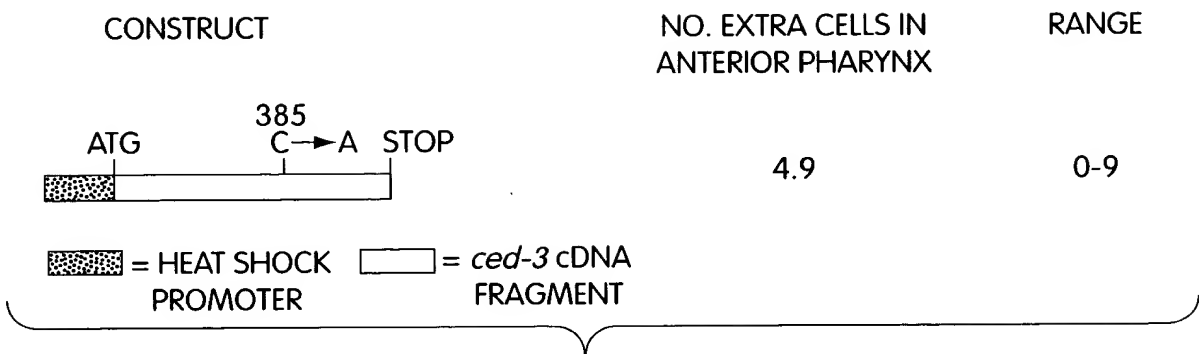


Fig. 10

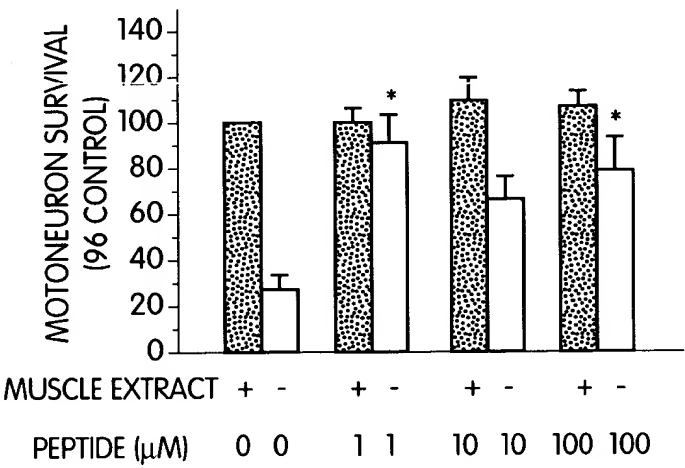


Fig. 11A

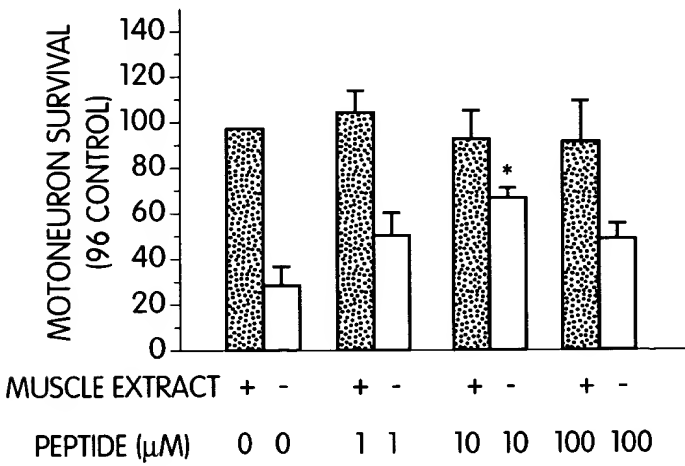


Fig. 11B

21/24

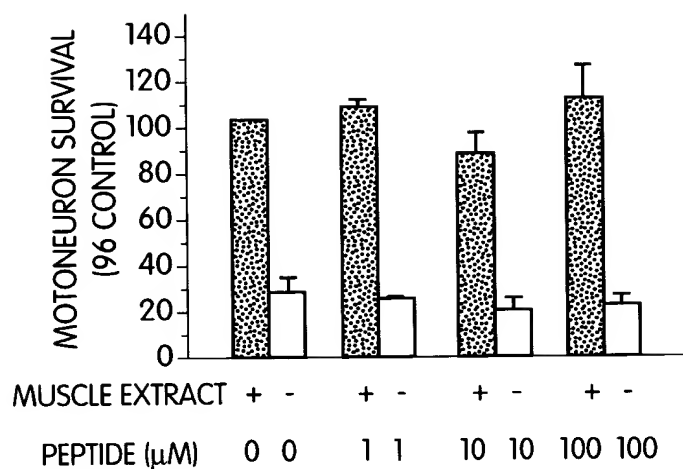


Fig. 11C

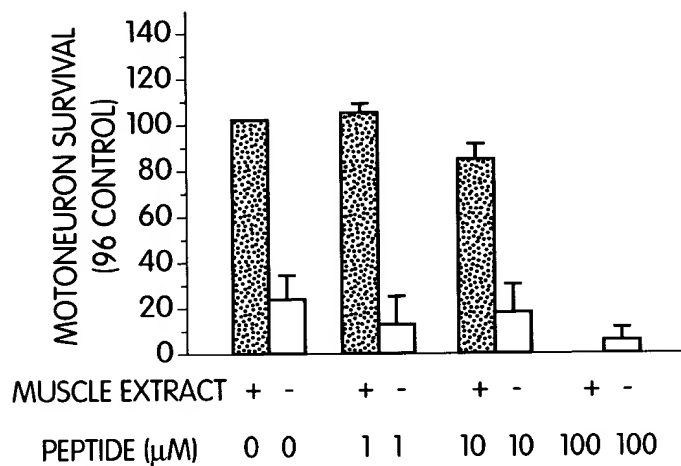


Fig. 11D

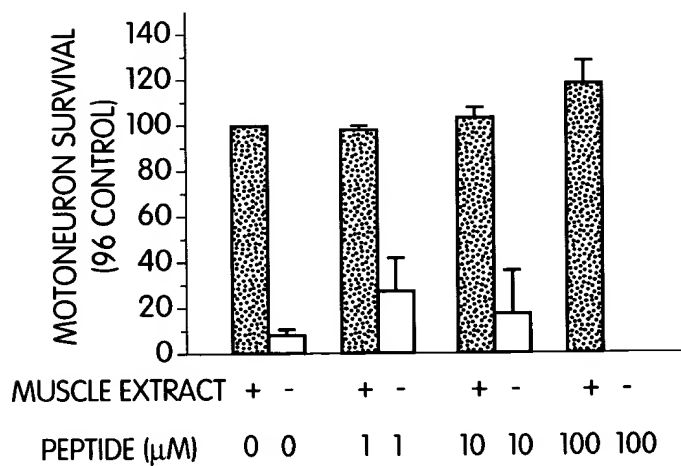
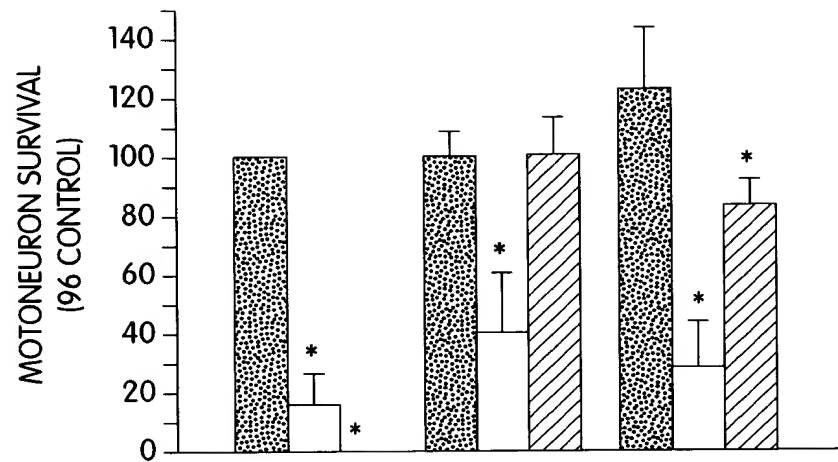
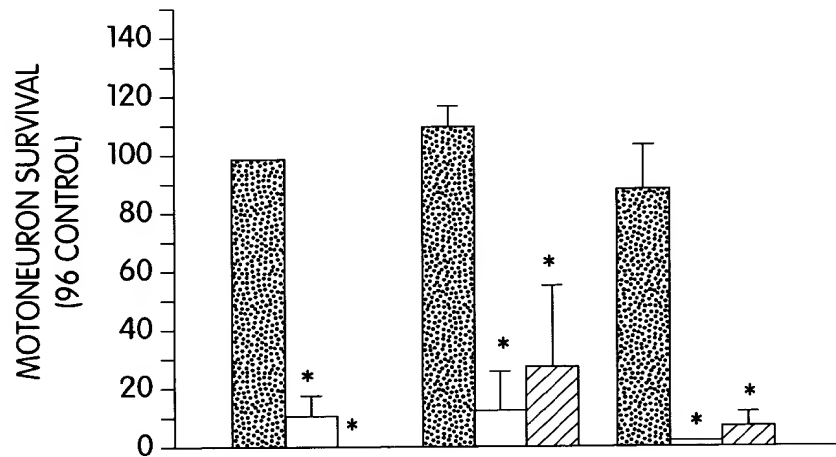


Fig. 11E



MUSCLE EXTRACT AT PLATING	+	-	-	+	-	-	+	-	-
PEPTIDE (μM)	0	0	0	1	1	1	10	10	10
MUSCLE EXTRACT AT 72 Hrs.	-	-	+	-	-	+	-	-	+

Fig. 12A



MUSCLE EXTRACT AT PLATING	+	-	-	+	-	-	+	-	-
PEPTIDE (μM)	0	0	0	1	1	1	10	10	10
MUSCLE EXTRACT AT 72 Hrs.	-	-	+	-	-	+	-	-	+

Fig. 12B

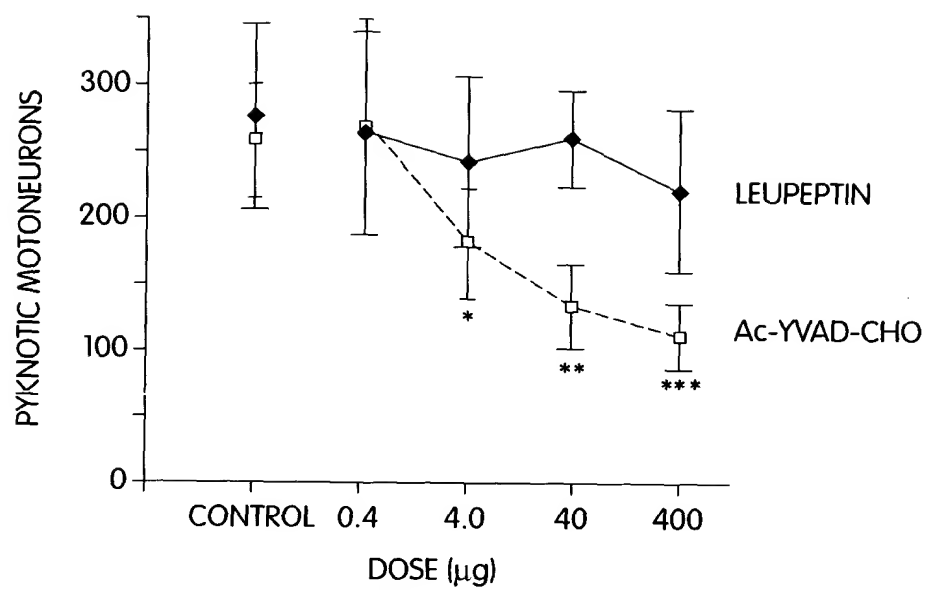


Fig. 13

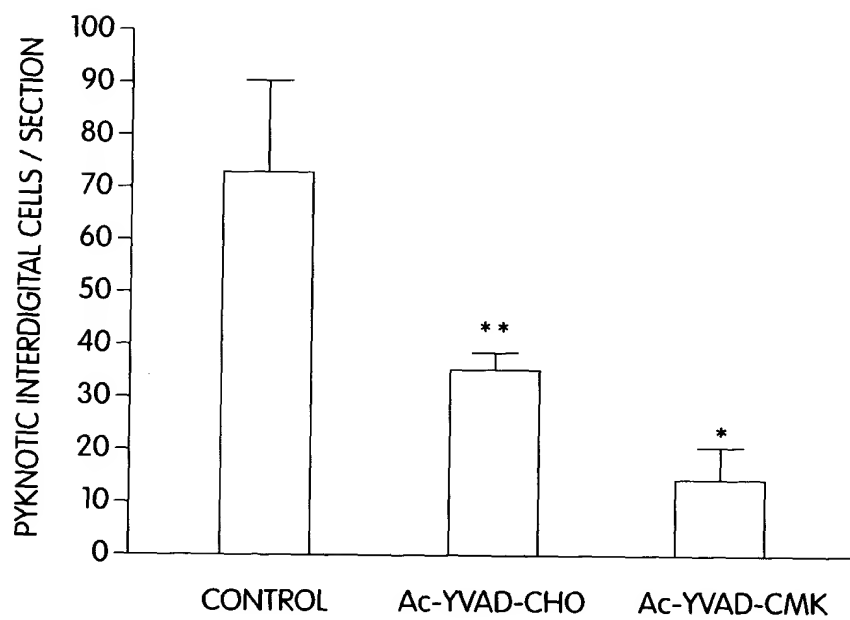


Fig. 14



Fig. 15C



Fig. 15D



Fig. 15E



Fig. 15F

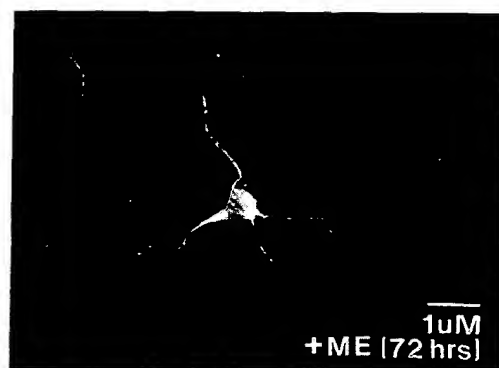


Fig. 15G

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